



## SEQUENCE LISTING

COPY OF PAPERS  
ORIGINALLY FILED

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<120> Methods of Controlling Gene Expression

<130> PB/5-31481A

<140> 09/896,186

<141> 2001-06-29

<160> 38

<170> PatentIn Ver. 2.1

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<213> Arabidopsis thaliana

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Lys Gly Phe Ala Lys Phe Gly Lys Ala Glu Val Pro Phe His Ile Pro
  35             40            45

Thr Leu Thr Lys Pro Gln Glu Tyr Lys Ile Leu Val Asp Asn Ala
  50             55            60

Asn Asn Pro Phe Glu His Val Leu Leu Glu Lys Ser Glu Asp Gly Leu
  65             70            75            80
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Leu Glu Asn Pro Gln Ile Glu Phe Gly Phe Leu Arg Gly Glu Cys Ser
      35             40             45

Leu Glu Met Ser Asp Ser Tyr Val Trp Val Glu Thr Glu Ser Gln Leu
      50             55             60

Lys Glu Leu Ala Glu Ile Leu Ala Lys Glu Gln Val Phe Ala Val Asp
      65             70             75             80

Thr Glu Gln His Ser Leu Arg Ser Phe Leu Gly Phe Thr Ala Leu Ile
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Gln Ile Ser Thr His Glu Glu Asp Phe Leu Val Asp Thr Ile Ala Leu
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His Asp Val Met Ser Ile Leu Arg Pro Val Phe Ser Asp Pro Asn Ile
      115            120            125

Cys Lys Val Phe His Gly Ala Asp Asn Asp Val Ile Trp Leu Gln Arg
      130            135            140

Asp Phe His Ile Tyr Val Val Asn Met Phe Asp Thr Ala Lys Ala Cys
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Glu Val Leu Ser Lys Pro Gln Arg Ser Leu Ala Tyr Leu Leu Glu Thr
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Val Cys Gly Val Ala Thr Asn Lys Leu Leu Gln Arg Glu Asp Trp Arg
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Gln Arg Pro Leu Ser Glu Glu Met Val Arg Tyr Ala Arg Thr Asp Ala  
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Tyr Ile Thr Lys Val Ile His Asp Cys Lys Arg Asp Ser Glu Ala Leu  
 35 40 45

Tyr Phe Gln Phe Gly Ile Arg Leu His Asn Val Val Asp Thr Gln Ile  
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Ala Tyr Ser Leu Ile Glu Glu Gln Glu Gly Arg Arg Arg Pro Leu Asp  
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Asp Tyr Ile Ser Phe Val Ser Leu Leu Ala Asp Pro Arg Tyr Cys Gly  
 85 90 95

Ile Ser Tyr Glu Glu Lys Glu Glu Val Arg Val Leu Met Arg Gln Asp  
 100 105 110  
 Pro Lys Phe Trp Thr Tyr Arg Pro Met Thr Glu Leu Met Ile Arg Ala  
 115 120 125  
 Ala Ala Asp Asp Val Arg Phe Leu Leu Tyr Leu Tyr His Lys Met Met  
 130 135 140  
 Gly Lys Leu Asn Gln Arg Ser Leu Trp His Leu Ala Val Arg Gly Ala  
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 165 170 175  
 Trp Pro Thr Val Pro Pro Ile Pro Val Phe Leu Val Lys Val Val Tyr  
 180 185 190  
 Ala Val Glu Thr Lys Lys Lys Arg Arg Val Thr Leu Ala Ser Ile Gly  
 195 200 205  
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 Glu Asp Gln Cys Leu Glu Glu Glu Ile Leu Ser Val Leu Asp Val Pro  
 225 230 235 240  
 Pro Gly Lys Met Gly Arg Val Ile Gly Arg Lys Gly Ala Ser Ile Leu  
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Val	Trp	Asn	Ser	Gln	Asp	Gln	Gly	Lys	Leu	Glu	Arg	Phe	Arg	His	Gln
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Arg	Ser	Leu	Ser	His	Asp	Gln	Ile	Val	Gln	Ala	Ser	Asp	Asp	Val	Tyr
			180					185					190		
Val	Cys	Cys	Lys	Leu	Gly	Val	Lys	Glu	Cys	Ile	Trp	Lys	Glu	Arg	Ser
		195					200					205			
Asn	Val	Lys	Glu	Arg	Ile	Trp	Lys	Glu	Ser	Ser	Asn	Val	Lys	Glu	His
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Trp Ile His Ser Ile Arg Phe Val Ser Arg Leu Arg Leu Ser His Pro
      50             55             60

Leu Val Val Gly Leu Gly Val Gln Trp Thr Pro Arg Gly Ser Asp Pro
      65             70             75             80

Pro Pro Asp Ile Leu Gln Leu Cys Val Gly Thr Arg Cys Leu Ile Ile
      85             90             95

Gln Leu Ser His Cys Lys Tyr Val Pro Asp Val Leu Arg Ser Phe Leu
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Glu Asp Gln Thr Ile Thr Phe Val Gly Val Trp Asn Ser Gln Asp Lys
      115            120            125

Asp Lys Leu Glu Arg Phe His His Gln Leu Asp Ile Trp Arg Leu Val
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His Ile Arg His Tyr Leu His Pro Leu Leu Leu Ser Ser Ser Phe Glu
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  65             70             75             80

Phe Asp Met Glu Trp Pro Pro Leu Tyr Asn Arg Gly Lys Leu Gly Lys
  85             90             95

Val Ala Leu Ile Gln Leu Cys Val Ser Glu Ser Lys Cys Tyr Leu Phe
 100             105             110

His Val Ser Ser Met Ser Val Phe Pro Gln Gly Leu Lys Met Leu Leu
 115             120             125

Glu Asn Lys Ala Val Lys Lys Ala Gly Val Gly Ile Glu Gly Asp Gln
 130             135             140

Trp Lys Leu Leu Arg Asp Phe Asp Ile Lys Leu Lys Asn Phe Val Glu
 145             150             155             160

Leu Thr Asp Val Ala Asn Lys Lys Leu Lys Cys Thr Glu Thr Trp Ser
 165             170             175

Leu Asn Ser Leu Val Lys His Leu Leu Gly Lys Gln Leu Leu Lys Asp
 180             185             190

Lys Ser Ile Arg Cys Ser Asn Trp Ser Lys Phe Pro Leu Thr Glu Asp

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210					215					220					
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225					230					235					240
Lys	Glu	Glu	Glu	Ile	Leu	Leu	Ser	Asp	Met	Asn	Lys	Gln	Leu	Thr	Ser
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Ile	Ser	Glu	Glu	Val	Met	Asp	Leu	Ala	Lys	His	Leu	Pro	His	Ala	Phe
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Ser	Lys	Leu	Glu	Asn	Pro	Arg	Arg	Val	Ser	Ile	Leu	Leu	Lys	Asp	Ile
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Ser	Glu	Asn	Leu	Tyr	Ser	Leu	Arg	Arg	Met	Ile	Ile	Gly	Ser	Thr	Asn
				290					295					300	
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Glu	Asp	Ser	Thr	Thr	Gly	Gly	Val	Gln	Gln	Lys	Gln	Ile	Arg	Glu	His
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Glu	Val	Leu	Ile	His	Val	Glu	Asp	Glu	Thr	Trp	Asp	Pro	Thr	Leu	Asp
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His	Leu	Ala	Lys	His	Asp	Gly	Glu	Asp	Val	Leu	Gly	Asn	Lys	Val	Glu
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Arg	Lys	Glu	Asp	Gly	Phe	Glu	Asp	Gly	Val	Glu	Asp	Asn	Lys	Leu	Lys
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Glu	Asn	Met	Glu	Arg	Ala	Cys	Leu	Met	Ser	Leu	Asp	Ile	Thr	Glu	His
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Glu	Leu	Gln	Ile	Leu	Glu	Gln	Gln	Ser	Gln	Glu	Glu	Tyr	Leu	Ser	Asp
				405					410					415	
Ile	Ala	Tyr	Lys	Ser	Thr	Glu	His	Leu	Ser	Pro	Asn	Asp	Asn	Glu	Asn
				420				425					430		
Asp	Thr	Ser	Tyr	Val	Ile	Glu	Ser	Asp	Glu	Asp	Leu	Glu	Met	Glu	Met
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Leu	Lys	His	Leu	Ser	Pro	Asn	Asp	Asn	Glu	Asn	Asp	Thr	Ser	Tyr	Val
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Asn	Leu	Asn	Ser	Gly	Thr	Val	Glu	Pro	Thr	His	Ser	Lys	Cys	Leu	Lys
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Met	Glu	Arg	Asn	Leu	Gly	Leu	Pro	Thr	Lys	Glu	Glu	Glu	Glu	Asp	Asp

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			580					585					590		
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Val	Thr	Pro	Glu	Tyr	Cys	Ser	Gly	Asn	Met	Gly	Leu	Leu	Gln	Gln	Leu
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Glu	Ala	Asp	Ile	Gly	Ile	Thr	Leu	Ile	Ala	Val	Asp	Glu	Ala	His	Cys
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Ile	Ser	Glu	Trp	Gly	His	Asp	Phe	Arg	Asp	Ser	Phe	Arg	Lys	Leu	Gly
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Ser	Leu	Lys	Thr	Ala	Leu	Pro	Met	Val	Pro	Ile	Val	Ala	Leu	Thr	Ala
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Thr	Ala	Ser	Ser	Ser	Ile	Arg	Glu	Asp	Ile	Val	Arg	Cys	Leu	Asn	Leu
705					710					715					720
Arg	Asn	Pro	Gln	Ile	Thr	Cys	Thr	Gly	Phe	Asp	Arg	Pro	Asn	Leu	Tyr
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Leu	Glu	Val	Arg	Arg	Lys	Thr	Gly	Asn	Ile	Leu	Gln	Asp	Leu	Gln	Pro
			740					745					750		
Phe	Leu	Val	Lys	Thr	Ser	Ser	His	Trp	Glu	Phe	Glu	Gly	Pro	Thr	Ile
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Arg	Lys	Leu	Asn	Leu	Ser	Cys	Gly	Thr	Tyr	His	Ala	Gly	Met	Ser	Phe
785					790					795					800
Ser	Thr	Arg	Lys	Asp	Ile	His	His	Arg	Phe	Val	Arg	Asp	Glu	Ile	Gln

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Cys	Val	Ile	Ala	Thr	Ile	Ala	Phe	Gly	Met	Gly	Ile	Asn	Lys	Ala	Asp
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Ile	Arg	Gln	Val	Ile	His	Tyr	Gly	Ala	Pro	Lys	Asp	Met	Glu	Ser	Tyr
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850				855				860							
His	Val	Leu	Trp	Ala	Pro	Ala	Asp	Ile	Asn	Leu	Asn	Arg	His	Leu	Leu
865				870				875				880			
Thr	Glu	Ile	Arg	Asn	Glu	Lys	Phe	Arg	Leu	Tyr	Lys	Leu	Lys	Met	Met
				885				890				895			
Ala	Lys	Met	Glu	Lys	Tyr	Leu	His	Ser	Ser	Arg	Cys	Arg	Arg	Gln	Ile
				900				905				910			
Ile	Leu	Ser	His	Phe	Glu	Asp	Lys	Gln	Val	Gln	Lys	Ala	Ser	Leu	Gly
915								920				925			
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930				935				940							
His	Cys	Tyr	Ser	Met	Asp	Asp	Ser	Glu	Asp	Thr	Ser	Trp	Asp	Phe	Gly
945				950				955				960			
Pro	Gln	Ala	Phe	Lys	Leu	Leu	Ser	Ala	Val	Asp	Ile	Leu	Gly	Glu	Lys
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				980				985				990			
Arg	Leu	Ala	Asp	Gln	Tyr	Arg	Arg	His	Ser	Leu	Phe	Gly	Thr	Gly	Lys
995				1000				1005							
Asp	Gln	Thr	Glu	Ser	Trp	Trp	Lys	Ala	Phe	Ser	Arg	Gln	Leu	Ile	Thr
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Glu	Gly	Phe	Leu	Val	Glu	Val	Ser	Arg	Tyr	Asn	Lys	Phe	Met	Lys	Ile
1025				1030				1035				1040			
Cys	Ala	Leu	Thr	Lys	Lys	Gly	Arg	Asn	Trp	Leu	His	Lys	Ala	Asn	Thr
				1045				1050				1055			
Glu	Ser	Gln	Ser	Leu	Ile	Leu	Gln	Ala	Asn	Glu	Glu	Leu	Cys	Pro	Lys
1060				1065				1070							
Lys	Phe	Leu	Leu	Pro	Ser	Ser	Lys	Thr	Val	Ser	Ser	Gly	Thr	Lys	Glu
1075				1080				1085							
His	Cys	Tyr	Asn	Gln	Val	Pro	Val	Glu	Leu	Ser	Thr	Glu	Lys	Lys	Ser
1090				1095				1100							
Asn	Leu	Glu	Lys	Leu	Tyr	Ser	Tyr	Lys	Pro	Cys	Asp	Lys	Ile	Ser	Ser

1105	1110	1115	1120
Gly Ser Asn Ile Ser Lys Lys Ser Ile Met Val Gln Ser Pro Glu Lys	1125	1130	1135
Ala Tyr Ser Ser Ser Gln Pro Val Ile Ser Ala Gln Glu Gln Glu Thr	1140	1145	1150
Gln Ile Val Leu Tyr Gly Lys Leu Val Glu Ala Arg Gln Lys His Ala	1155	1160	1165
Asn Lys Met Asp Val Pro Pro Ala Ile Leu Ala Thr Asn Lys Ile Leu	1170	1175	1180
Val Asp Met Ala Lys Met Arg Pro Thr Thr Val Glu Asn Val Lys Arg	1185	1190	1195
Ile Asp Gly Val Ser Glu Gly Lys Ala Ala Met Leu Ala Pro Leu Leu	1205	1210	1215
Glu Val Ile Lys His Phe Cys Gln Thr Asn Ser Val Gln Thr Asp Leu	1220	1225	1230
Phe Ser Ser Thr Lys Pro Gln Glu Glu Gln Lys Thr Ser Leu Val Ala	1235	1240	1245
Lys Asn Lys Ile Cys Thr Leu Ser Gln Ser Met Ala Ile Thr Tyr Ser	1250	1255	1260
Leu Phe Gln Glu Lys Lys Met Pro Leu Lys Ser Ile Ala Glu Ser Arg	1265	1270	1275
Ile Leu Pro Leu Met Thr Ile Gly Met His Leu Ser Gln Ala Val Lys	1285	1290	1295
Ala Gly Cys Pro Leu Asp Leu Glu Arg Ala Gly Leu Thr Pro Glu Val	1300	1305	1310
Gln Lys Ile Ile Ala Asp Val Ile Arg Asn Pro Pro Val Asn Ser Asp	1315	1320	1325
Met Ser Lys Ile Ser Leu Ile Arg Met Leu Val Pro Glu Asn Ile Asp	1330	1335	1340
Thr Tyr Leu Ile His Met Ala Ile Glu Ile Leu Lys His Gly Pro Asp	1345	1350	1355
Ser Gly Leu Gln Pro Ser Cys Asp Val Asn Lys Arg Arg Cys Phe Pro	1365	1370	1375
Gly Ser Glu Glu Ile Cys Ser Ser Ser Lys Arg Ser Lys Glu Glu Val	1380	1385	1390
Gly Ile Asn Thr Glu Thr Ser Ser Ala Glu Arg Lys Arg Arg Leu Pro	1395	1400	1405
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1410

1415

1420

Thr Lys Arg Gly Gly Leu Phe Ser  
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<220>  
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<210> 20  
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<210> 21  
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 cctgaaaaga aattgggttat cggttttgac tgtgaggggtg ttgacctctg ccgacatggg 180  
 aaactttgta tcatgcagat tgcattctct aatgcaatat acttggttga tgtcatcgaa 240  
 ggtggagagg tgattatgaa agcgtgtaag cctgcactcg agtctaatta catcacgaaa 300  
 gttattcacg attgcaagcg tgacagttag gctctatact tccagtttgg gataagattg 360  
 cacaatgttg tggacactca gattgcttat tctctgattg aagaacaaga agggcggagg 420  
 agacctctag atgattacat atcgtttgtt tcaactcctg ctgatccacg ttactgcggg 480  
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 aagaaaaaaa gacgggtgac attagcttcg attgggttac tgattgtagt tggactttta 840  
 aatgtggcag ataacctgaa gtcagaagat caatgtcttg aagaagagat cctgtcagtg 900  
 cttgatgttc caccaggaaa gatgggacgt gtgattggaa ggaaaggagc atcgatcctc 960  
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<400> 22

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			20					25					30			
Pro	Ala	Asp	Phe	Leu	Asn	Pro	Ser	Pro	Glu	Lys	Lys	Leu	Val	Ile	Gly	
		35					40					45				
Phe	Asp	Cys	Glu	Gly	Val	Asp	Leu	Cys	Arg	His	Gly	Lys	Leu	Cys	Ile	
	50					55					60					
Met	Gln	Ile	Ala	Phe	Ser	Asn	Ala	Ile	Tyr	Leu	Val	Asp	Val	Ile	Glu	
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Gly	Gly	Glu	Val	Ile	Met	Lys	Ala	Cys	Lys	Pro	Ala	Leu	Glu	Ser	Asn	
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Tyr	Ile	Thr	Lys	Val	Ile	His	Asp	Cys	Lys	Arg	Asp	Ser	Glu	Ala	Leu	
			100					105					110			
Tyr	Phe	Gln	Phe	Gly	Ile	Arg	Leu	His	Asn	Val	Val	Asp	Thr	Gln	Ile	
	115						120					125				
Ala	Tyr	Ser	Leu	Ile	Glu	Glu	Gln	Glu	Gly	Arg	Arg	Arg	Pro	Leu	Asp	
	130					135					140					
Asp	Tyr	Ile	Ser	Phe	Val	Ser	Leu	Leu	Ala	Asp	Pro	Arg	Tyr	Cys	Gly	
145					150					155					160	
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				165					170					175		
Pro	Lys	Phe	Trp	Thr	Tyr	Arg	Pro	Met	Thr	Glu	Leu	Met	Ile	Arg	Ala	
			180					185					190			
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		195					200					205				
Gly	Lys	Leu	Asn	Gln	Arg	Ser	Leu	Trp	His	Leu	Ala	Val	Arg	Gly	Ala	
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Leu	Tyr	Cys	Arg	Cys	Leu	Cys	Cys	Met	Asn	Asp	Ala	Asp	Phe	Ala	Asp	
225					230					235					240	
Trp	Pro	Thr	Val	Pro	Pro	Ile	Pro	Val	Phe	Leu	Val	Lys	Val	Val	Tyr	
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Ala	Val	Glu	Thr	Lys	Lys	Lys	Arg	Arg	Val	Thr	Leu	Ala	Ser	Ile	Gly	
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Leu Leu Ile Val Val Gly Leu Leu Asn Val Ala Asp Asn Leu Lys Ser  
 275 280 285

Glu Asp Gln Cys Leu Glu Glu Glu Ile Leu Ser Val Leu Asp Val Pro  
 290 295 300

Pro Gly Lys Met Gly Arg Val Ile Gly Arg Lys Gly Ala Ser Ile Leu  
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Ala Ile Lys Glu Ala Cys Asn Ala Glu Ile Leu Ile Gly Gly Ala Lys  
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Gly Pro Pro Asp Lys Val Ser Leu Ile Pro  
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<211> 1049

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ccgtccatgg	ccacgaggag	gatccaaatc	aaatcccca	taatatccgt	cgccaattgc	240
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gctcataacg	tgaaggagga	agcttaaagg	ttagcctata	acccaagag	ttagcatcaa	960
atgatatgat	acacctaata	tagtcaagta	gatgcaattc	ttgtgaatat	tgtatctagt	1020
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<211> 288

<212> PRT

<213> Arabidopsis thaliana

<400> 24

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Leu Ala Ile Asp Ala Ile Glu Ala Ser Tyr Asn Phe Ser Arg Ser Ser  
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Ser Ser Ser Ser Ser Ala Ala Pro Thr Val Gln Ala Thr Thr Ser Val  
 35 40 45



His Gly His Glu Glu Asp Pro Asn Gln Ile Pro Asn Asn Ile Arg Arg  
 50 55 60  
 Gln Leu Pro Arg Ser Ile Thr Ser Ser Thr Ser Tyr Lys Arg Phe Pro  
 65 70 75 80  
 Leu Ser Arg Cys Arg Ala Arg Asn Phe Pro Ala Met Arg Phe Gly Gly  
 85 90 95  
 Arg Ile Leu Tyr Ser Lys Thr Ala Thr Glu Val Asp Lys Arg Ala Met  
 100 105 110  
 Gln Leu Ile Lys Val Leu Asp Thr Lys Arg Asp Glu Ser Gly Ile Ala  
 115 120 125  
 Phe Val Gly Leu Asp Ile Glu Trp Arg Pro Ser Phe Arg Lys Gly Val  
 130 135 140  
 Leu Pro Gly Lys Val Ala Thr Val Gln Ile Cys Val Asp Ser Asn Tyr  
 145 150 155 160  
 Cys Asp Val Met His Ile Phe His Ser Gly Ile Pro Gln Ser Leu Gln  
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 His Leu Ile Glu Asp Ser Thr Leu Val Lys Val Gly Ile Gly Ile Asp  
 180 185 190  
 Gly Asp Ser Val Lys Leu Phe His Asp Tyr Gly Val Ser Ile Lys Asp  
 195 200 205  
 Val Glu Asp Leu Ser Asp Leu Ala Asn Gln Lys Ile Gly Gly Asp Lys  
 210 215 220  
 Lys Trp Gly Leu Ala Ser Leu Thr Glu Thr Leu Val Cys Lys Glu Leu  
 225 230 235 240  
 Leu Lys Pro Asn Arg Ile Arg Leu Gly Asn Trp Glu Phe Tyr Pro Leu  
 245 250 255  
 Ser Lys Gln Gln Leu Gln Tyr Ala Ala Thr Asp Ala Tyr Ala Ser Trp  
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<212> DNA

<213> Artificial Sequence

<220>

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<210> 31

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 TTACAGTATC AAGTTCATCG AGTTCTAGCT AATAAACCTC AACCAGGACC TGCTACTTTC 240  
 ATTATTAAT GTCTCACTTT ACTTCCTTTA TTTGGGGTAT ATGGTGAAGG CTTTAGTCAT 300  
 TTAGTTATAT CAGCTCTTCG CCGCTTCTTT AAAACAGTAT CTGAACCAAC TAGTGAAGAA 360  
 GATATTGTT TGGCGAGAAA GCTAGCTGCT CAGTTCTTCC TTGCTACTGT TGGTGGATCT 420  
 TTAACCTATG ATGAGAAGGT TATGGTGCAT ACTCTTAGAG TGTTTGATGT GAGGTAACT 480  
 AGTATCGATG AAGCCTTGTC TATCTCGGAA GTTTGGCAGA GATATGGGTT TGCTTGTGGA 540  
 AATGCGTTTC TGGACAATA CATTTCTGAC TTGATCAAGT CGAAATCTTT CATGACGGCT 600  
 GTGACTCTGT TAGAGCATTT CTCTTCCGT TTCCCTGGAG AAACCTTTCT TCAACAAATG 660  
 GTTGAGGATA AAAATTTCCA AGCTGCAGAG AGATGGGCTA CCTTCATGGG AAGGCCAAGT 720

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GCTCTGAAGG	TTCTAGCAGA	AAAAGCATGT	TGGGATGTTG	CTGAAATTAA	GACAAAAGGT	900
GATAGACAGC	TTCTGAAGTA	TCTGGTATAC	TTGGCAGTGG	AAGCTGGATA	CTTGGAGAAG	960
GTTGATGAAC	TGTGCGATCG	ATATTCACCT	CAAGGGCTGC	CAAAAGCACG	AGAGGCTGAG	1020
GTTGCTTTTG	TTGAAAAAAG	CTTTCTGCGT	CTCAACGATC	TAGCTGTAGA	AGATGTAGTT	1080
TGGGTTGATG	AAGTCAACGA	GTTGAGAAAA	GCAACTTCTT	TTCTTGAAGG	ATGTAGAGTT	1140
GTGGGTATTG	ACTGTGAATG	GAAACCTAAT	TATATTAAAG	GCAGTAAACA	GAACAAGGTT	1200
TCAATCATGC	AAATTGGATC	TGATACCAAA	ATTTTCATAT	TGGACTTGAT	AAAGCTTTAC	1260
AATGACGCCT	CTGAAATTCT	GGACAACTGC	CTTAGTCACA	TTTTGCAATC	GAAGAGTACA	1320
TAAAGCTCG	TCTCTCTGAC	TGAGGATTAC	CCTGATCATA	AATTATCCTC	AGGTTACAAT	1380
TTTCAATGTG	ACATCAAGCA	GTTGGCGCTT	TCATATGGGG	ATTTGAAATG	TTTCGAGCGA	1440
TACGACATGT	TGCTAGACAT	TCAAAATGTT	TTTAATGAAC	CATTTGGTGG	TTTAGCAGGA	1500
CTAACGAAGA	AAATATTGGG	AGTGTCTTTG	AACAAAACAA	GACGCAATAG	CGACTGGGAA	1560
CAAAGGCCTT	TGAGCCAGAA	TCAGCTTGAG	TATGCTGCTC	TTGATGCTGC	AGTGTTGATT	1620
CACATATTTT	GCCATGTTCG	CGATCATCCT	CCACATGACA	GTAGTTCAGA	GACAACCCAG	1680
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<212> PRT

<213> Arabidopsis thaliana

<400> 36

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			20					25						30	

Tyr	Val	Ser	Pro	Val	Val	Phe	Leu	Tyr	Leu	Leu	Lys	Glu	Cys	Tyr	Lys
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His	Gly	Ser	Leu	Lys	Ala	Thr	Lys	Lys	Phe	Gln	Ala	Leu	Gln	Tyr	Gln
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Val	His	Arg	Val	Leu	Ala	Asn	Lys	Pro	Gln	Pro	Gly	Pro	Ala	Thr	Phe
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Ile	Ile	Asn	Cys	Leu	Thr	Leu	Leu	Pro	Leu	Phe	Gly	Val	Tyr	Gly	Glu
				85					90					95	

Gly	Phe	Ser	His	Leu	Val	Ile	Ser	Ala	Leu	Arg	Arg	Phe	Phe	Lys	Thr
			100					105						110	

Val	Ser	Glu	Pro	Thr	Ser	Glu	Glu	Asp	Ile	Cys	Leu	Ala	Arg	Lys	Leu
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Ala	Ala	Gln	Phe	Phe	Leu	Ala	Thr	Val	Gly	Gly	Ser	Leu	Thr	Tyr	Asp
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Glu	Lys	Val	Met	Val	His	Thr	Leu	Arg	Val	Phe	Asp	Val	Arg	Leu	Thr
145					150					155					160

Ser	Ile	Asp	Glu	Ala	Leu	Ser	Ile	Ser	Glu	Val	Trp	Gln	Arg	Tyr	Gly
				165					170					175	

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180 185 190  
Lys Ser Lys Ser Phe Met Thr Ala Val Thr Leu Leu Glu His Phe Ser  
195 200 205  
Phe Arg Phe Pro Gly Glu Thr Phe Leu Gln Gln Met Val Glu Asp Lys  
210 215 220  
Asn Phe Gln Ala Ala Glu Arg Trp Ala Thr Phe Met Gly Arg Pro Ser  
225 230 235 240  
Leu Cys Ile Leu Val Gln Glu Tyr Gly Ser Arg Asn Met Leu Lys Gln  
245 250 255  
Ala Tyr Asn Ile Ile Asn Lys Asn Tyr Leu Gln His Asp Phe Pro Glu  
260 265 270  
Leu Tyr His Lys Cys Lys Glu Ser Ala Leu Lys Val Leu Ala Glu Lys  
275 280 285  
Ala Cys Trp Asp Val Ala Glu Ile Lys Thr Lys Gly Asp Arg Gln Leu  
290 295 300  
Leu Lys Tyr Leu Val Tyr Leu Ala Val Glu Ala Gly Tyr Leu Glu Lys  
305 310 315 320  
Val Asp Glu Leu Cys Asp Arg Tyr Ser Leu Gln Gly Leu Pro Lys Ala  
325 330 335  
Arg Glu Ala Glu Val Ala Phe Val Glu Lys Ser Phe Leu Arg Leu Asn  
340 345 350  
Asp Leu Ala Val Glu Asp Val Val Trp Val Asp Glu Val Asn Glu Leu  
355 360 365  
Arg Lys Ala Thr Ser Phe Leu Glu Gly Cys Arg Val Val Gly Ile Asp  
370 375 380  
Cys Glu Trp Lys Pro Asn Tyr Ile Lys Gly Ser Lys Gln Asn Lys Val  
385 390 395 400  
Ser Ile Met Gln Ile Gly Ser Asp Thr Lys Ile Phe Ile Leu Asp Leu  
405 410 415  
Ile Lys Leu Tyr Asn Asp Ala Ser Glu Ile Leu Asp Asn Cys Leu Ser  
420 425 430  
His Ile Leu Gln Ser Lys Ser Thr Leu Lys Leu Val Ser Leu Thr Glu  
435 440 445  
Asp Tyr Pro Asp His Lys Leu Ser Ser Gly Tyr Asn Phe Gln Cys Asp  
450 455 460  
Ile Lys Gln Leu Ala Leu Ser Tyr Gly Asp Leu Lys Cys Phe Glu Arg  
465 470 475 480

Tyr Asp Met Leu Leu Asp Ile Gln Asn Val Phe Asn Glu Pro Phe Gly  
 485 490 495  
 Gly Leu Ala Gly Leu Thr Lys Lys Ile Leu Gly Val Ser Leu Asn Lys  
 500 505 510  
 Thr Arg Arg Asn Ser Asp Trp Glu Gln Arg Pro Leu Ser Gln Asn Gln  
 515 520 525  
 Leu Glu Tyr Ala Ala Leu Asp Ala Ala Val Leu Ile His Ile Phe Arg  
 530 535 540  
 His Val Arg Asp His Pro Pro His Asp Ser Ser Ser Glu Thr Thr Gln  
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 Trp Lys Ser His Ile Val Ser Thr Ser Tyr Lys Ser Pro Tyr Leu Ser  
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 CACTCCAATA CGTCGTCGTT TCCGACCGTC ACTCTCCTCC AAGTCGCATG CCGACTCAGT 180  
 CACGCCACGG ATGTCTCCGA TGTCTTCCTC ATTGATTGTA GTTCGATTCA TCTTCCATCG 240  
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 AAGAAAACAA GAAGACGTGT CGCCTCAAGC ACTATGAACA CAAATAAGCA GTTGGTCTGT 960  
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 CAAAGAATAC CCAACTGCTT ATTTAACAAA AATTTAGAGT TTTGGCAGTG CATGAAGTGC 1440  
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			20					25					30			
Leu	Asp	Ala	Glu	Trp	Lys	Pro	Gln	His	Ser	Asn	Thr	Ser	Ser	Phe	Pro	
		35					40					45				
Thr	Val	Thr	Leu	Leu	Gln	Val	Ala	Cys	Arg	Leu	Ser	His	Ala	Thr	Asp	
	50					55					60					
Val	Ser	Asp	Val	Phe	Leu	Ile	Asp	Leu	Ser	Ser	Ile	His	Leu	Pro	Ser	
65					70					75					80	
Val	Trp	Glu	Leu	Leu	Asn	Asp	Met	Phe	Val	Ser	Pro	Asp	Val	Leu	Lys	
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Leu	Gly	Phe	Arg	Phe	Lys	Gln	Asp	Leu	Val	Tyr	Leu	Ser	Ser	Thr	Phe	
			100					105						110		
Thr	Gln	His	Gly	Cys	Glu	Gly	Gly	Phe	Gln	Glu	Val	Lys	Gln	Tyr	Leu	
		115					120						125			
Asp	Ile	Thr	Ser	Ile	Tyr	Asn	Tyr	Leu	Gln	His	Lys	Arg	Phe	Gly	Arg	
	130					135					140					
Lys	Ala	Pro	Lys	Asp	Ile	Lys	Ser	Leu	Ala	Ala	Ile	Cys	Lys	Glu	Met	
145					150					155					160	
Leu	Asp	Ile	Ser	Leu	Ser	Lys	Glu	Leu	Gln	Cys	Ser	Asp	Trp	Ser	Tyr	
				165					170					175		
Arg	Pro	Leu	Thr	Glu	Glu	Gln	Lys	Leu	Tyr	Ala	Ala	Thr	Asp	Ala	His	
			180					185					190			
Cys	Leu	Leu	Gln	Ile	Phe	Asp	Val	Phe	Glu	Ala	His	Leu	Val	Glu	Gly	
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225					230					235					240	
Lys	Ala	Thr	Asp	Val	Ile	Arg	Ser	Met	Ser	Glu	Asn	Gly	Gln	Asn	Ile	
				245					250					255		
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			260					265					270			
Asp	Glu	Asn	Leu	Leu	Lys	Ile	Val	Arg	Lys	Phe	Gly	Glu	Arg	Ile	Leu	
	275						280					285				
Leu	Lys	Glu	Ser	Asp	Leu	Leu	Pro	Lys	Lys	Leu	Lys	Lys	Lys	Thr	Arg	

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Arg	Arg	Val	Ala	Ser	Ser	Thr	Met	Asn	Thr	Asn	Lys	Gln	Leu	Val	Cys
305					310					315					320
Ser	Ala	Asp	Trp	Gln	Gly	Pro	Pro	Pro	Trp	Asp	Ser	Ser	Leu	Gly	Gly
				325					330					335	
Asp	Gly	Cys	Pro	Lys	Phe	Leu	Leu	Asp	Val	Met	Val	Glu	Gly	Leu	Ala
			340					345					350		
Lys	His	Leu	Arg	Cys	Val	Gly	Ile	Asp	Ala	Ala	Ile	Pro	His	Ser	Lys
		355					360					365			
Lys	Pro	Asp	Ser	Arg	Glu	Leu	Leu	Asp	Gln	Ala	Phe	Lys	Glu	Asn	Arg
	370					375					380				
Val	Leu	Leu	Thr	Arg	Asp	Thr	Lys	Leu	Leu	Arg	His	Gln	Asp	Leu	Ala
385						390					395				400
Lys	His	Gln	Ile	Tyr	Arg	Val	Lys	Ser	Leu	Leu	Lys	Asn	Glu	Gln	Leu
				405					410					415	
Leu	Glu	Val	Ile	Glu	Thr	Phe	Gln	Leu	Lys	Ile	Ser	Gly	Asn	Gln	Leu
			420					425					430		
Met	Ser	Arg	Cys	Thr	Lys	Cys	Asn	Gly	Lys	Phe	Ile	Gln	Lys	Pro	Leu
		435					440					445			
Ser	Ile	Glu	Glu	Ala	Ile	Glu	Ala	Ala	Lys	Gly	Phe	Gln	Arg	Ile	Pro
	450					455					460				
Asn	Cys	Leu	Phe	Asn	Lys	Asn	Leu	Glu	Phe	Trp	Gln	Cys	Met	Asn	Cys
465						470					475				480
His	Gln	Leu	Tyr	Trp	Glu	Gly	Thr	Gln	Tyr	His	Asn	Ala	Val	Gln	Lys
				485					490					495	
Phe	Met	Glu	Val	Cys	Lys	Leu	Ser	Glu							
			500					505							